



SEQUENCE LISTING

#4

<110> ZHU, JIAN-KANG

LIU, JIPING

ISHITANI, MANABU

HALFTER, URSULA

KIM, CHEOL-SOO

TOCTED
120> PROTEINS AND DNA RELATED TO SALT TOLERANCE IN PLANTS

130> 205645US20

140> 09/824,735

141> 2001-04-04

150> US 60/824,735

151> 2000-04-04

160> 16

170> PatentIn version 3.1

210> 1

211> 5144

212> DNA

213> Arabidopsis thaliana

<220>

<221> CDS

<222> (2004) .. (2168)

<223>

<220>

<221> CDS

<222> (2255) .. (2317)

<223>

<220>

<221> CDS

<222> (2416) .. (2487)

<223>

<220>

<221> CDS

<222> (2573) .. (2680)

<223>

<220>

<221> CDS

<222> (2778) .. (2852)

<223>

<220>

<221> CDS

<222> (2921) .. (3100)

<223>

<220>

<221> CDS

<222> (3225) .. (3314)

<223>

<220>

<221> CDS

<222> (3418) .. (3540)

<223>

<220>

<221> CDS

<222> (4052) .. (4171)

<223>

<220>

<221> CDS

<222> (4400) .. (4516)

<223>

<220>

<221> CDS

<222> (4735)..(4791)

<223>

<220>

<221> CDS

<222> (4879)..(4953)

<223>

<220>

<221> CDS

<222> (5038)..(5130)

<223>

<400> 1

tttttggcgg gaaaatctcg ggtttacgtt tttggcggga aaatctcgtg ttacggtttt 60
tggcgggaaa atctcgggtt tacgtttttt gcgagaaaat cacgggttta cttttttttg 120
cgggaaaatc acggatttat gtttttttgt ggaaaaatta cgagtttact ttttctcaat 180
ttcattgctt gtatatTTaa gaaatttgga aaaatattaa ttttattaaa ttggtttaga 240
tgtgttggtt aaacctaaat tggcatttgt ttagagattt tagttgggtt tattcaattt 300
tacaaaattt gatgggttaa ttggataaac catggaaacc attaaccatt acaacctaac 360
tcattttact catcaaacca attgactcat caactcattt gactcatcaa ctcatgtgag 420
tcaaaaattt caactcatta gggttcatgg gttgagttga gttgagttga cccatgaatt 480
ttgacccatt ttgacacccc tacatatgat cataagttaa taatcaaaaa ttactattga 540
taacttttta acggaattgt tttgtaagtt tcattttacgt tatttatata aaaaaacata 600
atgcaaaagt actaatgtat agttattttt atttttaata atgcaaaaat attactgtaa 660
tactttttca ttcttatcaa ttttttttct tatattcaat tagccaccaa cacctacatt 720
tcatatTTct cttcacattc attattttct tgctcttgta ttccttctta tcatcttcat 780

tgccaatttt	tcattgacat	tgatcatcgtt	actttgtatg	tatgattttt	gaacatttaa	840										
tgtgaatccc	aaccgactat	aggactatca	agaagttttc	aaacttttta	aaaaagatct	900										
tgaaccttta	aagcaaattcc	caaccgacta	tagaaccata	gtcctcttcc	ttgttgatga	960										
agctcttctc	gtgccggcga	aaatctaggc	cataaaaagcc	tcttcaacat	cacctagtat	1020										
attgaccgtg	accatctttt	tgaccattgc	tttgtgaatg	aaccgtcgat	aaaccgtggt	1080										
atcacttacg	ccaaattttt	ccctagtgtt	tgtttccaaa	ctctcacgaa	tccttatcga	1140										
acttttttat	atatcacttt	gtagcattgg	aaagtatctt	tgtatgcttt	gtcttaaact	1200										
tagacatcct	tgttctcttg	gtttttttga	accttgcttg	acttaaataga	agttaaaaaat	1260										
ttgtagttaa	aaatagaaaa	ttttactaat	ttgagttcga	ttaatcatag	tctagataat	1320										
ttgaaaaaaa	ttaaaataaa	ttttgaaaat	actatatgtt	tattttttta	aaataattta	1380										
ctaaattgat	aagtgatatt	agattagttt	tttttttctt	ttttaaattt	tgaaaacctc	1440										
aaattatta	aattgaaaga	ttcaaaatgc	aatgttagtt	tttaaaagtt	taatcaccca	1500										
aaacggataat	tgacccgaac	gactaattca	ggtcgtatac	gggtacagtc	aaataacccg	1560										
acccgaaatg	ctcaacggat	ctgcacggac	gttcgcacgc	acgattcacg	gctttcgcga	1620										
atcgcatcac	gagccttcct	tctctcctac	gcctctttca	tcaacccttc	tctgcgaatc	1680										
caattctggt	atttcacgat	tctctttcga	ctacgcccaa	tcgcaattcc	agccgtacga	1740										
attttatata	ttgattatga	tcttgatcct	taccttttcg	tcgtttcctt	gatcgaattt	1800										
atgttgattt	atgctgcgaa	atcaaaaatta	tggtacacaga	gtaattttgt	atatatggat	1860										
gtgtaggagc	taaaattagc	aaacaatacg	taaagtaatt	gaaatcgaaa	tcataaacgt	1920										
ttaaggaaaag	aggttttttac	taagtctctg	aataatctga	ttgatagctt	gtgggtcaatg	1980										
gatcagataa	aagttttgtaa	aga	atg	aca	aag	aaa	atg	aga	aga	gtg	ggc	aag	2033			
			Met	Thr	Lys	Lys	Met	Arg	Arg	Val	Gly	Lys				
			1				5					10				
tac	gag	ggt	ggt	cgc	aca	ata	ggt	gaa	gga	acc	ttt	gct	aag	ggt	aag	2081
Tyr	Glu	Val	Gly	Arg	Thr	Ile	Gly	Glu	Gly	Thr	Phe	Ala	Lys	Val	Lys	
				15					20					25		
ttt	gcg	agg	aac	aca	gac	act	ggt	gat	aat	gta	gcc	atc	aaa	att	atg	2129
Phe	Ala	Arg	Asn	Thr	Asp	Thr	Gly	Asp	Asn	Val	Ala	Ile	Lys	Ile	Met	
			30					35					40			

gct aag agt aca ata ctt aag aac aga atg gtt gat cag gtatgttctg	2178
Ala Lys Ser Thr Ile Leu Lys Asn Arg Met Val Asp Gln	
45 50 55	
gattgttttt tacatggaaa ctaagggttgt tgcgtcaatg gtatgatctt tgatttcggt	2238
taaagctctt ttacag ata aaa aga gag ata tct ata atg aag att gtt cgt	2290
Ile Lys Arg Glu Ile Ser Ile Met Lys Ile Val Arg	
60 65	
cac ccg aac ata gtg agg ttg tat gag gtatgtttgt ttgtttccat	2337
His Pro Asn Ile Val Arg Leu Tyr Glu	
70 75	
gcatactgcga aattttatct ctgaagtgtt tttgcatcat tgttcttctg ttgttttttt	2397
gtgattttcc cgatgtag gtg ttg gcg agt cct tcg aaa ata tat ata gtt	2448
Val Leu Ala Ser Pro Ser Lys Ile Tyr Ile Val	
80 85	
ttg gag ttt gtg aca gga gga gag ctc ttt gat aga att gtacggaact	2497
Leu Glu Phe Val Thr Gly Gly Glu Leu Phe Asp Arg Ile	
90 95 100	
tcataacttg taggcagcgt ccattagtta aaacctctct acttaatttt ttaatatatg	2557
aaatctttca tgcag gtt cat aaa ggg agg ctt gaa gaa agt gag tct cgg	2608
Val His Lys Gly Arg Leu Glu Glu Ser Glu Ser Arg	
105 110	
aaa tac ttt caa cag ctt gta gat gct gtt gct cat tgt cac tgc aag	2656
Lys Tyr Phe Gln Gln Leu Val Asp Ala Val Ala His Cys His Cys Lys	
115 120 125	
ggg gtt tac cac cgt gac cta aag gtaaagacgt gtttttggtt accaatattc	2710
Gly Val Tyr His Arg Asp Leu Lys	
130 135	
ctcagaatat ctcaactgcgt tgcaatccag acttgatatt tttgtgtcgc tatgttatgt	2770
tatctag cca gaa aat ctt tta ctc gat aca aat gga aat ctg aag gtt	2819
Pro Glu Asn Leu Leu Leu Asp Thr Asn Gly Asn Leu Lys Val	
140 145 150	
tcg gat ttc gga ctc agt gca ttg cct cag gaa gtaagtgtc ttatctctgc	2872
Ser Asp Phe Gly Leu Ser Ala Leu Pro Gln Glu	
155 160	
ttcagcagtc tgcttacgtg gtcattaact tgttatatac tcaatcag gga gta gaa	2929
Gly Val Glu	

ctt ctg cgt acc aca tgt gga act ccg aac tat gta gct cca gag gta	2977
Leu Leu Arg Thr Thr Cys Gly Thr Pro Asn Tyr Val Ala Pro Glu Val	
165 170 175 180	
ctt agt gga cag ggt tac gat ggt tca gca gct gat att tgg tct tgc	3025
Leu Ser Gly Gln Gly Tyr Asp Gly Ser Ala Ala Asp Ile Trp Ser Cys	
185 190 195	
ggg gtt att ctt ttc gtt ata ttg gct gga tat tta cct ttt tcc gag	3073
Gly Val Ile Leu Phe Val Ile Leu Ala Gly Tyr Leu Pro Phe Ser Glu	
200 205 210	
acg gat ctt cca ggg ttg tac aga aaa gtaagtaaca tatctttcgg	3120
Thr Asp Leu Pro Gly Leu Tyr Arg Lys	
215 220	
gagaaaatca tgaattcctt gtcattggctt ttgtcaaacc gtttattgat ttggttttgc	3180
atcttcacccc ttagtttttga gctttttacac attgtttattt acag ata aat gca gca	3236
Ile Asn Ala Ala	
225	
gag ttt tct tgt cca ccg tgg ttt tcc gca gaa gtg aag ttt tta ata	3284
Glu Phe Ser Cys Pro Pro Trp Phe Ser Ala Glu Val Lys Phe Leu Ile	
230 235 240	
gat agg ata ctt gac ccc aat ccc aaa aca gtgagtattt tgctttgttc	3334
His Arg Ile Leu Asp Pro Asn Pro Lys Thr	
245 250	
tctcctagct atcagggtttt ggtgatattt aatgtttctag taattatatc tgtttatcta	3394
ttattgtttc tcaattagag cag cgt att caa att caa gga atc aag aaa gat	3447
Arg Ile Gln Ile Gln Gly Ile Lys Lys Asp	
255 260	
cct tgg ttc aga tta aat tat gtg cct ata cga gca agg gaa gaa gaa	3495
Pro Trp Phe Arg Leu Asn Tyr Val Pro Ile Arg Ala Arg Glu Glu Glu	
265 270 275	
gaa gtg aat ttg gat gat att cgt gca gtt ttt gat gga att gag	3540
Glu Val Asn Leu Asp Asp Ile Arg Ala Val Phe Asp Gly Ile Glu	
280 285 290	
gtttgtgctt cgccttcatt atatgctctt tgctggtcaa ttccatttaa atgttaagat	3600
ctcttaggaa cgtttggtatg accaagaaga agtgtttgct acaggataga acaaaatagt	3660
aggcatgtgt tagttaccaa acctgtaaac tgcttcttta ttcaattcgc caaaccatag	3720
accttaggaa gacttagatt tacaagagaa ttctctattc tcgaccaaaa acctagaca	3780

aaatccagaa	taccctagg	gctaattaca	atgttcatgt	acctatcaat	atatatctcc		3840
tgctaagatt	gtcttagctt	tggtatagcc	tagatatata	tagataccgt	aattttcta		3900
gcataatttag	aatgttttac	ttaaactcag	gctcttgcte	ttctaaaact	tgtacttcaa		3960
ttgttaaaact	aaaacctcag	tatctgtctt	agctaaagtt	acttttactt	gttttttcatt		4020
aagttgacct	gtcaattgca	cttgttcaca	g ggc agt tat gta gcg gag aat				4072
			Gly Ser Tyr Val Ala Glu Asn				295
gta gag aga aat gat gaa ggg ccc ctg atg atg aat gcc ttt gag atg							4120
Val Glu Arg Asn Asp Glu Gly Pro Leu Met Met Asn Ala Phe Glu Met							
300		305		310		315	
att acc tta tca caa ggc tta aat tta tct gca cta ttt gac agg cga							4168
Ile Thr Leu Ser Gln Gly Leu Asn Leu Ser Ala Leu Phe Asp Arg Arg							
		320		325		330	
cag gtagtacctg atttttctatt actggtcata gagatctcca ttctgaataa							4221
Gln							
agaatgtcg gtagcatcta ttcttcagac tgcccgtttt gactgcctta tgatgctgtg							4281
ttcttagttt gttataataa ctataagttc attagatgat tggttgcatg gcattagtag							4341
atacaaatgg aatccaaaat gttcctgcat attgatggct gatcctttga tctcgcag							4399
gat ttt gtt aaa agg caa acc cgt ttt gtt tct cga agg gaa cct agt							4447
Asp Phe Val Lys Arg Gln Thr Arg Phe Val Ser Arg Arg Glu Pro Ser							
		335		340		345	
gag ata att gct aac att gag gct gta gcg aac tca atg ggt ttt aag							4495
Glu Ile Ile Ala Asn Ile Glu Ala Val Ala Asn Ser Met Gly Phe Lys							
350		355		360			
tct cat aca cga aac ttc aag gtaacgaatt cctagcatat tacacttatc							4546
Ser His Thr Arg Asn Phe Lys							
365		370					
acagagatta tgcattatTTT taaaactctc aactgttaaa cgcatgtgta gatagattga							4606
taagattgac aaggaaactt agttttatata tctggcggttc aaaaacgaaa gtcctagtg							4666
gaattatcat ttttaatggtt agcagagagt acaattgtta tgatttggtta cgtctatgtg							4726
ctcaacag aca agg ctC gag gga tta tct tcg atc aag gcc gga cag tta							4776
Thr Arg Leu Glu Gly Leu Ser Ser Ile Lys Ala Gly Gln Leu							
		375		380		385	

gct gtt gtg ata gag gtaattattg cttgttggtga ttgtaatatata agtttgcttt 4831
Ala Val Val Ile Glu
390

gcttcagttt aagggtatct agcaaattga aattaaccta catgcag att tac gag 4887
Ile Tyr Glu

gtg gca cca tcg ctt ttc atg gta gac gta aga aag gct gct ggt gaa 4935
Val Ala Pro Ser Leu Phe Met Val Asp Val Arg Lys Ala Ala Gly Glu
395 400 405

act ctt gaa tat cac aag gtttataaat atatatccaa taacaatagt 4983
Thr Leu Glu Tyr His Lys
410 415

tgcatcatta ctgtgttgcg gattagagtg atattttggtt ttgtggtatc gcag ttc 5040
Phe

tac aag aag cta tgt tcg aaa ctg gaa aac ata ata tgg agg gca aca 5088
Tyr Lys Lys Leu Cys Ser Lys Leu Glu Asn Ile Ile Trp Arg Ala Thr
420 425 430

gaa gga ata cca aag tca gag att ctc aga aca atc acg ttt 5130
Glu Gly Ile Pro Lys Ser Glu Ile Leu Arg Thr Ile Thr Phe
435 440 445

tgatcccaac ttaa 5144

<210> 2

<211> 446

<212> PRT

<213> Arabidopsis thaliana

<400> 2

Met Thr Lys Lys Met Arg Arg Val Gly Lys Tyr Glu Val Gly Arg Thr
1 5 10 15

Ile Gly Glu Gly Thr Phe Ala Lys Val Lys Phe Ala Arg Asn Thr Asp
20 25 30

Thr Gly Asp Asn Val Ala Ile Lys Ile Met Ala Lys Ser Thr Ile Leu

35

40

45

Lys Asn Arg Met Val Asp Gln Ile Lys Arg Glu Ile Ser Ile Met Lys
50 55 60

Ile Val Arg His Pro Asn Ile Val Arg Leu Tyr Glu Val Leu Ala Ser
65 70 75 80

Pro Ser Lys Ile Tyr Ile Val Leu Glu Phe Val Thr Gly Gly Glu Leu
85 90 95

Phe Asp Arg Ile Val His Lys Gly Arg Leu Glu Glu Ser Glu Ser Arg
100 105 110

Lys Tyr Phe Gln Gln Leu Val Asp Ala Val Ala His Cys His Cys Lys
115 120 125

Gly Val Tyr His Arg Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Thr
130 135 140

Asn Gly Asn Leu Lys Val Ser Asp Phe Gly Leu Ser Ala Leu Pro Gln
145 150 155 160

Glu Gly Val Glu Leu Leu Arg Thr Thr Cys Gly Thr Pro Asn Tyr Val
165 170 175

Ala Pro Glu Val Leu Ser Gly Gln Gly Tyr Asp Gly Ser Ala Ala Asp
180 185 190

Ile Trp Ser Cys Gly Val Ile Leu Phe Val Ile Leu Ala Gly Tyr Leu
195 200 205

Pro Phe Ser Glu Thr Asp Leu Pro Gly Leu Tyr Arg Lys Ile Asn Ala
210 215 220

Ala Glu Phe Ser Cys Pro Pro Trp Phe Ser Ala Glu Val Lys Phe Leu
225 230 235 240

Ile His Arg Ile Leu Asp Pro Asn Pro Lys Thr Arg Ile Gln Ile Gln

245

250

255

Gly Ile Lys Lys Asp Pro Trp Phe Arg Leu Asn Tyr Val Pro Ile Arg
 260 265 270

Ala Arg Glu Glu Glu Glu Val Asn Leu Asp Asp Ile Arg Ala Val Phe
 275 280 285

Asp Gly Ile Glu Gly Ser Tyr Val Ala Glu Asn Val Glu Arg Asn Asp
 290 295 300

Glu Gly Pro Leu Met Met Asn Ala Phe Glu Met Ile Thr Leu Ser Gln
 305 310 315 320

Gly Leu Asn Leu Ser Ala Leu Phe Asp Arg Arg Gln Asp Phe Val Lys
 325 330 335

Arg Gln Thr Arg Phe Val Ser Arg Arg Glu Pro Ser Glu Ile Ile Ala
 340 345 350

Asn Ile Glu Ala Val Ala Asn Ser Met Gly Phe Lys Ser His Thr Arg
 355 360 365

Asn Phe Lys Thr Arg Leu Glu Gly Leu Ser Ser Ile Lys Ala Gly Gln
 370 375 380

Leu Ala Val Val Ile Glu Ile Tyr Glu Val Ala Pro Ser Leu Phe Met
 385 390 395 400

Val Asp Val Arg Lys Ala Ala Gly Glu Thr Leu Glu Tyr His Lys Phe
 405 410 415

Tyr Lys Lys Leu Cys Ser Lys Leu Glu Asn Ile Ile Trp Arg Ala Thr
 420 425 430

Glu Gly Ile Pro Lys Ser Glu Ile Leu Arg Thr Ile Thr Phe
 435 440 445

<210> 3

<211> 633

<212> PRT

<213> Saccharomyces cerevisiae

<400> 3

Met Ser Ser Asn Asn Asn Thr Asn Thr Ala Pro Ala Asn Ala Asn Ser
1 5 10 15

Ser His His His His His His His His His His His His Gly His
20 25 30

Gly Gly Ser Asn Ser Thr Leu Asn Asn Pro Lys Ser Ser Leu Ala Asp
35 40 45

Gly Ala His Ile Gly Asn Tyr Gln Ile Val Lys Thr Leu Gly Glu Gly
50 55 60

Ser Phe Gly Lys Val Lys Leu Ala Tyr His Thr Thr Thr Gly Gln Lys
70 75 80

Val Ala Leu Lys Ile Ile Asn Lys Lys Val Leu Ala Lys Ser Asp Met
85 90 95

Gln Gly Arg Ile Glu Arg Glu Ile Ser Tyr Leu Arg Leu Leu Arg His
100 105 110

Pro His Ile Ile Lys Leu Tyr Asp Val Ile Lys Ser Lys Asp Glu Ile
115 120 125

Ile Met Val Ile Glu Tyr Ala Gly Asn Glu Leu Phe Asp Tyr Ile Val
130 135 140

Gln Arg Asp Lys Met Ser Glu Gln Glu Ala Arg Arg Phe Phe Gln Gln
145 150 155 160

Ile Ile Ser Ala Val Glu Tyr Cys His Arg His Lys Ile Val His Arg
165 170 175

Asp Leu Lys Pro Glu Asn Leu Leu Leu Asp Glu His Leu Asn Val Lys
 180 185 190

Ile Ala Asp Phe Gly Leu Ser Asn Ile Met Thr Asp Gly Asn Phe Leu
 195 200 205

Lys Thr Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser
 210 215 220

Gly Lys Leu Tyr Ala Gly Pro Glu Val Asp Val Trp Ser Cys Gly Val
 225 230 235 240

Ile Leu Tyr Val Met Leu Cys Arg Arg Leu Pro Phe Asp Asp Glu Ser
 245 250 255

Ile Pro Val Leu Phe Lys Asn Ile Ser Asn Gly Val Tyr Thr Leu Pro
 260 265 270

Lys Phe Leu Ser Pro Gly Ala Ala Gly Leu Ile Lys Arg Met Leu Ile
 275 280 285

Val Asn Pro Leu Asn Arg Ile Ser Ile His Glu Ile Met Gln Asp Asp
 290 295 300

Trp Phe Lys Val Asp Leu Pro Glu Tyr Leu Leu Pro Pro Asp Leu Lys
 305 310 315 320

Pro His Pro Glu Glu Glu Asn Glu Asn Asn Asp Ser Lys Lys Asp Gly
 325 330 335

Ser Ser Pro Asp Asn Asp Glu Ile Asp Asp Asn Leu Val Asn Ile Leu
 340 345 350

Ser Ser Thr Met Gly Tyr Glu Lys Asp Glu Ile Tyr Glu Ser Leu Glu
 355 360 365

Ser Ser Glu Asp Thr Pro Ala Phe Asn Glu Ile Arg Asp Ala Tyr Met
 370 375 380

Leu Ile Lys Glu Asn Lys Ser Leu Ile Lys Asp Met Lys Ala Asn Lys
 385 390 395 400

Ser Val Ser Asp Glu Leu Asp Thr Phe Leu Ser Gln Ser Pro Pro Thr
 405 410 415

Phe Gln Gln Gln Ser Lys Ser His Gln Lys Ser Gln Val Asp His Glu
 420 425 430

Thr Ala Lys Gln His Ala Arg Arg Met Ala Ser Ala Ile Thr Gln Gln
 435 440 445

Arg Thr Tyr His Gln Ser Pro Phe Met Asp Gln Tyr Lys Glu Glu Asp
 450 455 460

Ser Thr Val Ser Ile Leu Pro Thr Ser Leu Pro Gln Ile His Arg Ala
 465 470 475 480

Asn Met Leu Ala Gln Gly Ser Pro Ala Ala Ser Lys Ile Ser Pro Leu
 485 490 495

Val Thr Lys Lys Ser Lys Thr Arg Trp His Phe Gly Ile Arg Ser Arg
 500 505 510

Ser Tyr Pro Leu Asp Val Met Gly Glu Ile Tyr Ile Ala Leu Lys Asn
 515 520 525

Leu Gly Ala Glu Trp Ala Lys Pro Ser Glu Glu Asp Leu Trp Thr Ile
 530 535 540

Lys Leu Arg Trp Lys Tyr Asp Ile Gly Asn Lys Thr Asn Thr Asn Glu
 545 550 555 560

Lys Ile Pro Asp Leu Met Lys Met Val Ile Gln Leu Phe Gln Ile Glu
 565 570 575

Thr Asn Asn Tyr Leu Val Asp Phe Lys Phe Asp Gly Trp Glu Ser Ser
 580 585 590

Tyr Gly Asp Asp Thr Thr Val Ser Asn Ile Ser Glu Asp Glu Met Ser
595 600 605

Thr Phe Ser Ala Tyr Pro Phe Leu His Leu Thr Thr Lys Leu Ile Met
610 615 620

Glu Leu Ala Val Asn Ser Gln Ser Asn
625 630

<210> 4

<211> 552

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly His Tyr
5 10 15

Val Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val Lys Ile
20 25 30

Gly Glu His Gln Leu Thr Gly His Lys Val Ala Val Lys Ile Leu Asn
35 40 45

Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Lys Arg Glu
50 55 60

Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr
65 70 75 80

Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val
85 90 95

Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu
100 105 110

Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp
 115 120 125

Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn
 130 135 140

Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu
 145 150 155 160

Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser
 165 170 175

Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly
 180 185 190

Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu
 195 200 205

Cys Gly Thr Leu Pro Phe Asp Asp Glu His Val Pro Thr Leu Phe Lys
 210 215 220

Lys Ile Arg Gly Gly Val Phe Tyr Ile Pro Glu Tyr Leu Asn Arg Ser
 225 230 235 240

Val Ala Thr Leu Leu Met His Met Leu Gln Val Asp Pro Leu Lys Arg
 245 250 255

Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln Gly Leu
 260 265 270

Pro Ser Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Asp Ala Asn Val Ile
 275 280 285

Asp Asp Glu Ala Val Lys Glu Val Cys Glu Lys Phe Glu Cys Thr Glu
 290 295 300

Ser Glu Val Met Asn Ser Leu Tyr Ser Gly Asp Pro Gln Asp Gln Leu
 305 310 315 320

Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met Asn Gln
325 330 335

Ala Ser Glu Phe Tyr Leu Ala Ser Ser Pro Pro Ser Gly Ser Phe Met
340 345 350

Asp Asp Ser Ala Met His Ile Pro Pro Gly Leu Lys Pro His Pro Glu
355 360 365

Arg Met Pro Pro Leu Ile Ala Asp Ser Pro Lys Ala Arg Cys Pro Leu
370 375 380

Asp Ala Leu Asn Thr Thr Lys Pro Lys Ser Leu Ala Val Lys Lys Ala
385 390 395 400

Lys Trp His Leu Gly Ile Arg Ser Gln Ser Lys Pro Tyr Asp Ile Met
405 410 415

Ala Glu Val Tyr Arg Ala Met Lys Gln Leu Asp Phe Glu Trp Lys Val
420 425 430

Val Asn Ala Tyr His Leu Arg Val Arg Arg Lys Asn Pro Val Thr Gly
435 440 445

Asn Tyr Val Lys Met Ser Leu Gln Leu Tyr Leu Val Asp Asn Arg Ser
450 455 460

Tyr Leu Leu Asp Phe Lys Ser Ile Asp Asp Glu Val Val Glu Gln Arg
465 470 475 480

Ser Gly Ser Ser Thr Pro Gln Arg Ser Cys Ser Ala Ala Gly Leu His
485 490 495

Arg Pro Arg Ser Ser Phe Asp Ser Thr Thr Ala Glu Ser His Ser Leu
500 505 510

Ser Gly Ser Leu Thr Gly Ser Leu Thr Gly Ser Thr Leu Ser Ser Val
515 520 525

Ser Pro Arg Leu Gly Ser His Thr Met Asp Phe Phe Glu Met Cys Ala
 530 535 540

Ser Leu Ile Thr Thr Leu Ala Arg
 545 550

<210> 5

<211> 496

<212> PRT

<213> Schizosaccharomyces pombe

<400> 5

Met Ala Gln Lys Leu Asp Asn Phe Pro Tyr His Ile Gly Arg Glu Ile
 5 10 15

Gly Thr Gly Ala Phe Ala Ser Val Arg Leu Cys Tyr Asp Asp Asn Ala
 20 25 30

Lys Ile Tyr Ala Val Lys Phe Val Asn Lys Lys His Ala Thr Ser Cys
 35 40 45

Met Asn Ala Gly Val Trp Ala Arg Arg Met Ala Ser Glu Ile Gln Leu
 50 55 60

His Lys Leu Cys Asn Gly His Lys Asn Ile Ile His Phe Tyr Asn Thr
 65 70 75 80

Ala Glu Asn Pro Gln Trp Arg Trp Val Val Leu Glu Phe Ala Gln Gly
 85 90 95

Gly Asp Leu Phe Asp Lys Ile Glu Pro Asp Val Gly Ile Asp Glu Asp
 100 105 110

Val Ala Gln Phe Tyr Phe Ala Gln Leu Met Glu Gly Ile Ser Phe Met
 115 120 125

His Ser Lys Gly Val Ala His Arg Asp Leu Lys Pro Glu Asn Ile Leu
130 135 140

Leu Asp Tyr Asn Gly Asn Leu Lys Ile Ser Asp Phe Gly Phe Ala Ser
145 150 155 160

Leu Phe Ser Tyr Lys Gly Lys Ser Arg Leu Leu Asn Ser Pro Val Gly
165 170 175

Ser Pro Pro Tyr Ala Ala Pro Glu Ile Thr Gln Gln Tyr Asp Gly Ser
180 185 190

Lys Val Asp Val Trp Ser Cys Gly Ile Ile Leu Phe Ala Leu Leu Leu
195 200 205

Gly Asn Thr Pro Trp Asp Glu Ala Ile Ser Asn Thr Gly Asp Tyr Leu
210 215 220

Leu Tyr Lys Lys Gln Cys Glu Arg Pro Ser Tyr His Pro Trp Asn Leu
225 230 235 240

Leu Ser Pro Gly Ala Tyr Ser Ile Ile Thr Gly Met Leu Arg Ser Asp
245 250 255

Pro Phe Lys Arg Tyr Ser Val Lys His Val Val Gln His Pro Trp Leu
260 265 270

Thr Ser Ser Thr Pro Phe Arg Thr Lys Asn Gly Asn Cys Ala Asp Pro
275 280 285

Val Ala Leu Ala Ser Arg Leu Met Leu Lys Leu Arg Ile Asp Leu Asp
290 295 300

Lys Pro Arg Leu Ala Ser Ser Arg Ala Ser Gln Asn Asp Ser Gly Phe
305 310 315 320

Ser Met Thr Gln Pro Ala Phe Lys Lys Asn Asp Gln Lys Glu Leu Asp
325 330 335

Arg Val Glu Val Tyr Gly Ala Leu Ser Gln Pro Val Gln Leu Asn Lys
 340 345 350

Asn Ile Asp Val Thr Glu Ile Leu Glu Lys Asp Pro Ser Leu Ser Gln
 355 360 365

Phe Cys Glu Asn Glu Gly Phe Ile Lys Arg Leu Ala Lys Lys Ala Lys
 370 375 380

Asn Phe Tyr Glu Ile Cys Pro Pro Glu Arg Leu Thr Arg Phe Tyr Ser
 385 390 395 400

Arg Ala Ser Arg Glu Thr Ile Ile Asp His Leu Tyr Asp Ser Leu Arg
 405 410 415

Leu Leu Ala Ile Ser Val Thr Met Lys Tyr Val Arg Asn Gln Thr Ile
 420 425 430

Leu Tyr Val Asn Leu His Asp Lys Arg Lys Cys Leu Leu Gln Gly Val
 435 440 445

Ile Glu Leu Thr Asn Leu Gly His Asn Leu Glu Leu Ile Asn Phe Ile
 450 455 460

Lys Arg Asn Gly Asp Pro Leu Glu Trp Arg Lys Phe Phe Lys Asn Val
 465 470 475 480

Val Ser Ser Ile Gly Lys Pro Ile Val Leu Thr Asp Val Ser Gln Asn
 485 490 495

<210> 6

<211> 476

<212> PRT

<213> Homo sapiens

<400> 6

Met Ala Val Pro Phe Val Glu Asp Trp Asp Leu Val Gln Thr Leu Gly
1 5 10 15

Glu Gly Ala Tyr Gly Glu Val Gln Leu Ala Val Asn Arg Val Thr Glu
20 25 30

Glu Ala Val Ala Val Lys Ile Val Asp Met Lys Arg Ala Val Asp Cys
35 40 45

Pro Glu Asn Ile Lys Lys Glu Ile Cys Ile Asn Lys Met Leu Asn His
50 55 60

Glu Asn Val Val Lys Phe Tyr Gly His Arg Arg Glu Gly Asn Ile Gln
65 70 75 80

Tyr Leu Phe Leu Glu Tyr Cys Ser Gly Gly Glu Leu Phe Asp Arg Ile
85 90 95

Glu Pro Asp Ile Gly Met Pro Glu Pro Asp Ala Gln Arg Phe Phe His
100 105 110

Gln Leu Met Ala Gly Val Val Tyr Leu His Gly Ile Gly Ile Thr His
115 120 125

Arg Asp Ile Lys Pro Glu Asn Leu Leu Leu Asp Glu Arg Asp Asn Leu
130 135 140

Lys Ile Ser Asp Phe Gly Leu Ala Thr Val Phe Arg Tyr Asn Asn Arg
145 150 155 160

Glu Arg Leu Leu Asn Lys Met Cys Gly Thr Leu Pro Tyr Val Ala Pro
165 170 175

Glu Leu Leu Lys Arg Arg Glu Phe His Ala Glu Pro Val Asp Val Trp
180 185 190

Ser Cys Gly Ile Val Leu Thr Ala Met Leu Ala Gly Glu Leu Pro Trp
195 200 205

Asp Gln Pro Ser Asp Ser Cys Gln Glu Tyr Ser Asp Trp Lys Glu Lys
210 215 220

Lys Thr Tyr Leu Asn Pro Trp Lys Lys Ile Asp Ser Ala Pro Leu Ala
225 230 235 240

Leu Leu His Lys Ile Leu Val Glu Asn Pro Ser Ala Arg Ile Thr Ile
245 250 255

Pro Asp Ile Lys Lys Asp Arg Trp Tyr Asn Lys Pro Leu Lys Lys Gly
260 265 270

Ala Lys Arg Pro Arg Val Thr Ser Gly Gly Val Ser Glu Ser Pro Ser
275 280 285

Gly Phe Ser Lys His Ile Gln Ser Asn Leu Asp Phe Ser Pro Val Asn
290 295 300

Ser Ala Ser Ser Glu Glu Asn Val Lys Tyr Ser Ser Ser Gln Pro Glu
305 310 315 320

Pro Arg Thr Gly Leu Ser Leu Trp Asp Thr Ser Pro Ser Tyr Ile Asp
325 330 335

Lys Leu Val Gln Gly Ile Ser Phe Ser Gln Pro Thr Cys Pro Asp His
340 345 350

Met Leu Leu Asn Ser Gln Leu Leu Gly Thr Pro Gly Ser Ser Gln Asn
355 360 365

Pro Trp Gln Arg Leu Val Lys Arg Met Thr Arg Phe Phe Thr Lys Leu
370 375 380

Asp Ala Asp Lys Ser Tyr Gln Cys Leu Lys Glu Thr Cys Glu Lys Leu
385 390 395 400

Gly Tyr Gln Trp Lys Lys Ser Cys Met Asn Gln Val Thr Ile Ser Thr
405 410 415

Thr Asp Arg Arg Asn Asn Lys Leu Ile Phe Lys Val Asn Leu Leu Glu
 420 425 430

Met Asp Asp Lys Ile Leu Val Asp Phe Arg Leu Ser Lys Gly Asp Gly
 435 440 445

Leu Glu Phe Lys Arg His Phe Leu Lys Ile Lys Gly Lys Leu Ile Asp
 450 455 460

Ile Val Ser Ser Gln Lys Val Trp Leu Pro Ala Thr
 465 470 475

<210> 7

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 7

gcggatccat gacaaagaaa atgagaagag tgggc

35

<210> 8

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 8

attgtactct tagccataat gttgatggct

30

<210> 9

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 9

gcgaattctt aagttgggat caaaacgtga ttgttctg

38

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 10

gtgataatgt agccatcaac attatggcta

30

<210> 11

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 11

gcggatccat gacaaagaaa atgagaagag tgggc

35

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 12
atataacgaa aagaataacc tcgcaagacc

30

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 13
gctgatattt ggtcttgcga gggtattctt

30

<210> 14

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 14

gcgaattcctt aagttgggat caaaacgtga ttgttctg

38

<210> 15

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 15

gggatccat gacaaagaaa atgagaagag tgggc

35

<210> 16

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic DNA

<400> 16

gcgaattcctt aagttgggat caaaacgtga ttgttctg

38